

AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

Claims 1-15. (Canceled)

16. (Previously Presented) The method according to claim 35, wherein the HBV genotype A specific target sequence in the HBsAg region is selected from the HBsAg region of the group consisting of SEQ ID NOs: 279-283.

Claim 17. (Canceled)

18. (Withdrawn – Currently Amended) The method according to claim 35 or claim 16, ~~characterized further by~~ further comprising a step of determining the presence or absence of HBV genotype B, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype B specific target sequence in the HBsAg region, wherein the HBV genotype B specific target sequence is SEQ ID NO:78, or the complement thereof.

Claim 19. (Canceled)

20. (Withdrawn - Currently Amended) The method according to claim 35 or claim 16, ~~characterized further by~~ further comprising a step of determining the presence or absence of HBV genotype C, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype C specific target sequence, wherein the HBV genotype C specific target sequence is selected from the group consisting of SEQ ID NO:153, SEQ ID NO:154 and SEQ ID NO:204, or the complement thereof.

Claim 21. (Canceled)

22. (Withdrawn - Currently Amended) The method according to claim 35 or claim 16, ~~characterized further by~~ further comprising a step of determining the presence or

absence of HBV genotype D, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype D specific target sequence, wherein the HBV genotype D specific target is selected from the group consisting of SEQ ID NO:165 and SEQ ID NO:208, or the complement thereof.

Claim 23. (Canceled)

24. (Withdrawn - Currently Amended) The method according to claim 35 or claim 16, ~~characterized further by~~ comprising a step of determining the presence or absence of HBV genotype E, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype E specific target sequence, wherein the HBV genotype E specific target sequence is selected from the group consisting of SEQ ID NO:172 and SEQ ID NO:213, or the complement thereof.

Claim 25. (Canceled)

26. (Withdrawn - Currently Amended) The method according to claim 35 or claim 16, ~~characterized further by~~ further comprising a step of determining the presence or absence of HBV genotype F, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype F specific target sequence, wherein the HBV genotype F specific target sequence is selected from the group consisting of SEQ ID NO:186, SEQ ID NO:216 and SEQ ID NO:219, or the complement thereof.

Claim 27. (Canceled)

28. (Previously Presented) The method according to claim 35 or claim 16 wherein the primer is selected from the group consisting of SEQ ID NOs: 75-76, 94, 104, 105, 112 and 134-135.

29. (Previously Presented) The method according to claim 35 or claim 16 wherein step (iii) is a reverse hybridization step.

Claim 30. (Canceled)

Claim 31. (Canceled)

Claim 32. (Canceled)

Claim 33. (Canceled)

Claim 34. (Canceled)

35. (Currently Amended) A method for determining the presence or absence of HBV genotype A in a biological sample, comprising:

- (i) providing a biological sample comprising polynucleic acids;
- (ii) optionally releasing, isolating and/or concentrating the polynucleic acids present in the sample;
- (iii) optionally amplifying the HBsAg region, or part thereof, of the HBV gene present in said sample with at least one primer pair;
- (iv) hybridizing the polynucleic acids of step (i) or (ii) or (iii) with at least one nucleotide probe selected from the group consisting of a sequence of 5-17 nucleotides long of SEQ ID NO 77, a sequence of 5-19 nucleotides long of SEQ ID NO 140, and a sequence of 5-18 nucleotides long of SEQ ID NO 193;
- (v) detecting the hybrid(s) formed in step (iv);
- (vi) inferring the HBV genotype present in said sample from the hybridization signal(s) obtained in step (v).

36. (Previously Presented) A method for determining the presence or absence of HBV genotype A in a biological sample, comprising:

- (i) providing a biological sample comprising polynucleic acids;
- (ii) optionally releasing, isolating and/or concentrating the polynucleic acids present in the sample;
- (iii) amplifying the HBsAg region, or part thereof, of the HBV gene present in said sample with at least one suitable primer pair, at least one primer of said primer pair being selected from the group consisting of SEQ ID NOs: 75, 76, 94, 104, 105, 112 and 134-135;
- (iv) hybridizing under stringent conditions the polynucleic acids of step (iii) with at least one nucleotide probe of about 5 to 50 nucleotides long hybridizing specifically to a HBV genotype A specific target sequence in the HBsAg region of HBV selected from the HBsAg region of the group consisting of SEQ ID NOs: 279-283;
- (v) detecting the hybrid(s) formed in step (iv);
- (vi) inferring the HBV genotype present in said sample from the hybridization signal(s) obtained in step (v).

Claim 37. (Canceled)

Claim 38. (Canceled)

39. (Previously Presented) The method according to claim 36 wherein step (iii) is a reverse hybridization step.

Claim 40. (Canceled)